

FASTA searches a protein or DNA sequence data bank
version 3.3t05 March 30, 2000

Please cite:

W.R. Pearson & D.J. Lipman PNAS (1988) 85:2444-2448

/tmp/fastaCAA0eaa3V: 3753 nt
>hSEC_6
vs /tmp/fastaDAA1eaa3V library
searching /tmp/fastaDAA1eaa3V library

4550 residues in 1 sequences

FASTA (3.34 January 2000) function [optimized, +5/-4 matrix (5:-4)] ktup: 6
join: 91, opt: 76, gap-pen: -16/ -4, width: 16
Scan time: 0.116

The best scores are:

					opt
gi 27435854 gb AF216967.1	Homo sapiens putati	(4550)	[f]	11374	
gi 27435854 gb AF216967.1	Homo sapiens putati	(4550)	[r]	72	

>>gi|27435854|gb|AF216967.1| Homo sapiens putative vascu (4550 nt)
initn: 11373 initl: 11373 opt: 11374
94.317% identity in 2534 nt overlap (1220-3753:1552-4085)

	1190	1200	1210	1220	1230	1240
hSEC_6	CTGTTACTAACAGAATCGATAAACAAAGGAATGATGGAATTATCTATAGAATATCCGTAG					
gi 274	CCAGCTGTGCAGACCTGGGGACCCTCTGTCAAGATGGAATTATCTATAGAATATCCGTAG					
	1530	1540	1550	1560	1570	1580

	1250	1260	1270	1280	1290	1300
hSEC_6	TGATTTCAGAACATCCTTCGTCACCCTGAGGTAAAAGTACAGAGCAAGGTGGCAGAATGGC					
gi 274	TGATTTCAGAACATCCTTCGTCACCCTGAGGTAAAAGTACAGAGCAAGGTGGCAGAATGGC					
	1590	1600	1610	1620	1630	1640

	1310	1320	1330	1340	1350	1360
hSEC_6	TCAATTCAACCTTCCAAAATTGGAAGTACACGGTTTATGTCGTTAATATCAGTTTTCACC					
gi 274	TCAATTCAACCTTCCAAAATTGGAAGTACACGGTTTATGTCGTTAATATCAGTTTTCACC					
	1650	1660	1670	1680	1690	1700

	1370	1380	1390	1400	1410	1420
hSEC_6	TGAGTGCTGGAGAGGACAAGATTAAAGTCAAGAGAAGCCTTGAGGATGAGCCAAGGTTGG					
gi 274	TGGGTGCTGGAGAGGACAAGATTAAAGTCAAGAGAAGCCTTGAGGATGAGCCAAGGTTGG					
	1710	1720	1730	1740	1750	1760

	1430	1440	1450	1460	1470	1480
hSEC_6	TGCTTTGGGCCCTTCTAGTTTACAATGCTACCAACAATACTAATTTAGAAGGAAAAATCA					
gi 274	TGCTTTGGGCCCTTCTAGTTTACAATGCTACCAACAATACTAATTTAGAAGGAAAAATCA					
	1770	1780	1790	1800	1810	1820

	1490	1500	1510	1520	1530	1540
hSEC_6	TTCAGCAGAAGCTCCTAAAAAATAATGAGTCCCTGGATGAAGGCTTGAGGCTACATACAG					
gi 274	TTCAGCAGAAGCTCCTAAAAAATAATGAGTCCCTGGATGAAGGCTTGAGGCTACATACAG					
	1830	1840	1850	1860	1870	1880

	1550	1560	1570	1580	1590	1600
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<http://bioinformatics.lexgen.com/tools/fasta3.php3>

<http://bioinformatics.lexgen.com/tools/fasta3.php3>

```
hSEC_6 TAGATGGCTGGATCACCTCCTTCAATGTGGATGGACTTTGCATTGCTGTTGCAGTCCTGT
: :::::::::::::::::::::::::::::::::::::: :: :::::::::: ::::
gi|274 TGGATGGCTGGATCACCTCCTTCAATGTGGATGGACTCTGCACCGCCGTTGCAGCCCTGC
      3090      3100      3110      3120      3130      3140

      2810      2820      2830      2840      2850      2860
hSEC_6 TGCATTTCTTCCTTCTGGCAACCTTTACCTGGATGGGGCTAGAAGCAATTCACATGTACA
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gi|274 TGCATTTCTTCCTTCTGGCAACCTTTACCTGGATGGGGCTAGAAGCAATTCACATGTACA
      3150      3160      3170      3180      3190      3200

      2870      2880      2890      2900      2910      2920
hSEC_6 TTGCTCTAGTTAAAGTATTTAACTTACATTGCGCGATACATTCTAAAATTCTGCATCA
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gi|274 TCGCTCTGGTTAAAGTTTTTAACACTTACATTGCGCGATACATACTGAAATTCTGCATCC
      3210      3220      3230      3240      3250      3260

      2930      2940      2950      2960      2970      2980
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: :::::::::: :::::::::::::: :::: :::::::::::::::::::::: ::::
gi|274 TTGGCTGGGGTCTGCCTGCCTTAGTTGTGTCCATTGTTCTAGCGAGCAGAAACCAAAATG
      3270      3280      3290      3300      3310      3320

      2990      3000      3010      3020      3030      3040
hSEC_6 AAGTCTATGGAAAAGAAAGTTATGGGAAAAGAAAGGTGATGAATTCTGTTGGATTCAAG
: :::::::::::::: :::::::::: :::: :::::::::::::::::::::: ::::
gi|274 AAGTCTATGGAAAAGAGAGTTATGGAAAAGAAAGGTGATGAATTCTGTTGGATTCAAG
      3330      3340      3350      3360      3370      3380

      3050      3060      3070      3080      3090      3100
hSEC_6 ATCCAGTCATATTTTATGTGACCTGTGCTGGGTATTTTGAGTCATGTTTTTCTGAACA
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gi|274 ATCCAGTCATATTTTATGTGACCTGTGCTGGGTATTTTGAGTCATGTTTTTCTGAACA
      3390      3400      3410      3420      3430      3440

      3110      3120      3130      3140      3150      3160
hSEC_6 TTGCCATGTTTCATTGTGGTAATGGTGCAGATCTGTGGGAGGAATGGCAAGAGAAGCAACC
: :::::::::::::::::::::::::::::::::::::: :::::::::::::: ::::
gi|274 TTGCCATGTTTCATTGTGGTAATGGTGCAGATCTGTGGGAGGAATGGCAAGAGAAGCAACC
      3450      3460      3470      3480      3490      3500

      3170      3180      3190      3200      3210      3220
hSEC_6 GGACCCTGAGAGAAGAAGTGTTAAGGAACCTGCGCAGTGTGGTTAGCTTGACCTTTCTGT
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gi|274 GGACCCTGAGAGAAGAAGTGTTAAGGAACCTGCGCAGTGTGGTTAGCTTGACCTTTCTGT
      3510      3520      3530      3540      3550      3560

      3230      3240      3250      3260      3270      3280
hSEC_6 TGGGCATGACATGGGGTTTTGCATTCTTTGCCTGGGGACCCTTAAATATCCCCTTCATGT
: :::::::::::::::::::::::::::::::::::::: :::::::::::::: ::::
gi|274 TGGGCATGACATGGGGTTTTGCATTCTTTGCCTGGGGACCCTTAAATATCCCCTTCATGT
      3570      3580      3590      3600      3610      3620

      3290      3300      3310      3320      3330      3340
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: :::::::::::::: :::::::::: :::: :::::::::::::::::::::: ::::
gi|274 ACCTCTTCTCCATCTTCAATTCATTACAAGGCTTATTTATATTCATCTTCCACTGTGCTA
      3630      3640      3650      3660      3670      3680

      3350      3360      3370      3380      3390      3400
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8/29/2003

3753 residues in 1 query sequences
4550 residues in 1 library sequences
Scomplib [version 3.3t05 March 30, 2000]
start: Fri Aug 29 16:19:07 2003 done: Fri Aug 29 16:19:08 2003
Scan time: 0.116 Display time: 0.200

Function used was FASTA

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DFESGQMDPLASVILPPNLENLSEEDSVLVKRAQFTFFNKTGLFQDVETQKGTLSVY
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DSDTNQTICLCNHLTHFGVLMDLPRASQLDAKNTKVLTFITYIGCGISAIKSAATLL
TYVAFEKLRRDYPKILMNLSALLFLNLIFLLDGWITSFNVDGLCTAVAALLHFFLL
ATFTWMGLEAIIHMYIALVKVFNTYIRRYILKFCILGWGLPALVVSIVLASRNQNEVYG
KESYGKEQGDEFQWIDPVIYFVTCAGYFGVMFFLNIAFIVVMVQICGRNGKRSNRT
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MKENVQKQWRRHLCCGRFRLADNSDWSKTATNIIKSSDNLGKSLSSSSSIGSNSTYLT
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NFYKNIIMSDTFSSHSTKF"

BASE COUNT 1310 a 1030 c 957 g 1253 t
ORIGIN

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61 ggcgaggacc tgcgacgcgc acccctgcct ggcccgtct cctcagcacc agccccacgc
121 acaccctact tctcagctt ctgcctctca cctgccaac ttccctgcga ggagggacct
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601 caaacagcca ggcttgcagc tggacgctcc gacgcccac cggttatatc attcagataa
661 catttaacga ctttgacatt gaagaagctc ccaattgcat ttatgactca ttatcccttg
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4501 aaatgtaact attttgaatg ccgaaaaaaa aaaaaaaaaa aaaaaaaaaa

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Aug 6 2003 13:17:41